

ABSTRACT

The present invention provides methods for analyzing exon expression profiles of a cell or type of cell. In the invention, the expression levels of a plurality of individual exons or multiexons for each of a plurality of genes in the genome of an organism are measured and analyzed to determine the biological state, such as the exon expression state or transcriptional state, of the cell or type of cell. The methods of the invention are useful for determination of alternative RNA splicing in a plurality of genes. The invention also provides nucleic acid probe arrays for determining in parallel the expression levels of a plurality of exons or multiexons for each of a plurality of genes in the genome of an organism. Such nucleic acid arrays comprise polynucleotide probes complementary and hybridizable to sequences in individual exons or multiexons. Methods for designing and making such nucleic acid probe arrays are also provided. The invention further provides methods for determining the effects of perturbations, such as perturbations by drugs, on exon expression and alternative RNA splicing pathways.

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